Summary of the Invention.

Page 5, line 7, replace the heading with the following new heading:

Brief Description of the Drawings.

Page 6, line 25, replace the heading with the following new heading:

Description of the Preferred Embodiments.

Page 26, replace the paragraph beginning at line 28 with the following paragraph:

A2

Analysis of N-terminus amino acid sequence of the band subjected to the blotting was carried out by Edman degradation method using HP G1005A Protein Sequencing System (HEWLETT PACKARD). As a result, it was revealed that the N-terminus amino acid sequence was

SLLAPLAPLRAHAGTRLTQG (SEQ ID NO: 7).

Based on this, DNA primers

NmaRout CCYTGIGTIARICKIGTICCIGCRTGIGCICG (SEQ ID NO: 8).

NmaRin CCIGCRTGIGCICGIARIGGIGCIARIGGIGC (SEQ ID NO: 9).

were designed, and PCR was carried out on the genome DNA of F. lutescens IFO 3084 strain using LA PCR in vitro cloning KIT (Takara Company). The PCR reaction condition was 30 cycles of 94°C, 30 seconds→55°C, 2 minutes→72°C, 1 minute. As a result, a PCR amplification fragment of about 400 bp containing the above terminus and its upstream region was obtained. Based on this sequence, its neighborhood region was obtained by using PCR. Namely, the genome DNA of F. lutescens IFO 3084 strain was digested with restriction enzymes PstI and

SalI, respectively, and the digests were subjected, respectively, to self-ligation reaction using Ligation Kit version 2 (Takara Company), and the resulting DNAs were used as template DNAs. Based on these template DNAs, DNA primers

A2 cont.

NIFout ttgatttgag cagattcgca ctgccattt (SEQ ID NO: 3)

NIRout aaggttttcg acaaagtgac catttccca (SEQ ID NO: 4)

were designed, and PCR was carried out using LA Taq (Takara Company). The PCR reaction condition was 30 cycles of 98°C, 20 seconds-68°C, 6 minutes. As a result, a PCR amplification fragment of about 2 kbp was obtained from the PstI template and a PCR amplification fragment of about 8 kbp from the SalI template. The base sequence was determined by the primer walking method using ABIPRISM 377XL DNA Sequencer (Perkin Elmer corporation) on these PCR amplification fragments. This base sequence is shown in SEQ ID NO: 1.

In the Abstract:

Page 34, line 1, replace the heading with the following new heading

ABSTRACT OF THE DISCLOSURE.

In The Sequence Listing:

Please replace the Sequence Listing of record with the attached substitute Sequence Listing.